

**Amendments to the Specification**

Please replace the paragraph beginning at page 7, line 32, with the following:

--Figure 4 shows sequence details of pBAR-EDN (SEQ ID NOS:1-3).--

Please replace the paragraph beginning at page 23, line 21, with the following:

--Modified forms of ONCONASE®, including humanized ONCONASE®, and recombinant ONCONASE® (rOnc) with a variety of activating modifications are described in copending U.S. Provisional Patent Application USSN 60/011,800 filed February 21, 1996 by Rybak *et al.* Preferred rOnc molecules have an amino terminal end selected from the group consisting of: Met-Ala; Met-Arg; Met-(J); Met-Lys-(J); Met-Arg-(J); Met-Lys; Met-Lys-Pro; ~~Met-Lys-(J)-Pro~~ Met-Lys-(J)-Pro (SEQ ID NO:4); Met-Lys-Pro-(J) (SEQ ID NO:5); Met-Asn; Met-Gln; Met-Asn-(J); Met-Gln-(J); Met-Asn-(J)-Pro (SEQ ID NO:6); Met-(J)-Lys; Met-(J)-Lys-Pro (SEQ ID NO:7) and Met-(J)-Pro-Lys (SEQ ID NO:8); where (J) is Ser, Tyr or Thr. In alternative forms of the rOnc molecules, the molecules employ an amino terminal end encoded by a sequence derived from the amino terminal end of EDN followed by a sequence from rOnc. In such forms, it is preferred that the amino acid sequence is one selected from the group consisting of those sequences substantially identical to those of a formula:  
Met(-1)EDN<sub>(1-m)</sub>Onc<sub>(n-104)</sub>; wherein Met(-1) refers to an amino terminal residue of Met; wherein EDN<sub>(1-m)</sub> refers to a contiguous sequence of amino acids of a length beginning at amino acid position 1 of EDN and continuing to and including amino acid position "m" of EDN; wherein Onc<sub>(n-104)</sub> refers to a sequence of contiguous amino acids beginning at amino acid position "n" and continuing to and including amino acid position 104 such that: when m is 21, n is 16 or 17; when m is 22, n is 17; when m is 20, n is 16; when m is 19, n is 15; when m is 18, n is 14; when m is 17, n is 12 or 13; when m is 16, n is 11, 12, 13 or 14; when m is 15, n is 10; when m is 14, n is 9; when m is 13, n is 8; and when m is 5, n is 1. *See*, USSN 60/011,800.--

Please replace the paragraph beginning at page 40, line 11, with the following:

--SU3: 5'-AAAAGGCCTCCCGGGACTGGAAGGGCTAATTCACT-3' (SEQ ID NO:9). The bases corresponding to nt. 16-35 in the LW/C viral sequence are underlined; the SmaI site is bold; sense orientation.

EU5AS: 5'-CCGGAATTCACCAGTCGCCGCCCTCGCC-3' (SEQ ID NO:10). The bases corresponding to nt. 744-763 in the LW/C viral sequence are underlined; the EcoRI site is bold; antisense orientation.

EU5S: 5'-CCGGAATTCGCCAAAAAATTTTGACTAGCG-3' (SEQ ID NO:11). The bases corresponding to nt. 770-790 in the LW/C viral sequence are underlined; the EcoRI site is bold; sense orientation.

XDGAS: 5[[1]]'-GGATCTAGATCTAGATTGCCCCCTATCATTATTGT-3' (SEQ ID NO:12). The bases corresponding to nt. 2284-2305 in the HXB2 viral sequence are underlined; the XbaI sites are bold; the stop codons are double underlined; antisense orientation.

SRRES: 5'-GGACGCGTCGACACCATTAGGAGTAGCACCCAC-3' (SEQ ID NO:13). The bases corresponding to nt. 7698-7717 in the HXB2 viral sequence are underlined; the SalI site is bold; sense orientation.

BLU5AS: 5'-CGCGGATCCACTGACTAAAAGGGTCTGAG-3' (SEQ ID NO:14). The bases corresponding to nt. 9681-9700 in the HXB2 viral sequence are underlined; the BamHI site is bold; antisense orientation.

ENVA: 5[[1]]'-AGAAATATCAGCACTTGTGGAGA-3' (SEQ ID NO:15). The sequence ~~correspond~~ corresponds to nt. 6237-6259 in the HXB2 viral sequence; sense orientation.

ENVB: 5[[1]]'-TGAGTGGCCCAAACATTATGTACCT-3' (SEQ ID NO:16). The sequence ~~correspond~~ corresponds to nt. 6414-6438 in the HXB2 viral sequence; antisense orientation.

ENVC: 5'-CACCCTCTATTTTGTGCATCAGATG-3' (SEQ ID NO:17). The sequence ~~correspond~~ corresponds to nt. 6369-6395 in the HXB2 viral sequence; sense orientation.

IRESA: 5'-GCTCTAGAGGAATTCCGCCCCTC-3' (SEQ ID NO:18). The XbaI site is bold; the EcoRI site is underlined; sense orientation (5' of the sequence).

IRESB: ~~[[3]]~~5'-GACTAGTGGCAAGCTTATCATCGTG-3' (SEQ ID NO:19)~~[[;]]~~. The SpeI site is bold; antisense orientation (3' of the sequence).

EDN $\alpha$ : 5'-CGCGGATCCTTGATATGCTGAGTTTCGAACCA-3' (SEQ ID NO:20). Sense orientation.

EDN $\omega$ : 5'-AAGGAAAAAAGCGGCCGCCTACTAGATGATACGGTCCAGA-3' (SEQ ID NO:21). Antisense orientation.

ECOSPL: 5'-GGGCGGCGACTGGTGAATT-3' (SEQ ID NO:22). Corresponding to nt. 750-768 in the pLW/C sequence. The nucleotides in bold correspond to the mutated nucleotides, with respect to pLW/C, present in pBAR and pBAR-EDN plasmids after the introduction of the ~~ECORI~~ EcoRI site. Sense orientation.

OTESAPL: 5'-TCTAACACTTCTCTCTCCGGGT-3' (SEQ ID NO:23). Corresponding to nt. 9317-9339 in the pHXB2 sequence. Antisense orientation. ~~oligonucleotides~~ Oligonucleotides 516, 477, 569F,  $\beta$ GS and  $\beta$ GAS have been described (Cara, *et al.*; *Virology*, **208**, 242-248 (1995)).--

Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 11, at the end of the application.

Appl. No. 09/230,195  
Amdt. dated April 16, 2004  
Amendment under 37 CFR 1.116 Expedited Procedure  
Examining Group 1633

PATENT

**Amendments to the Drawings**

Please replace the seven sheets of drawings with the accompanying eight replacement sheets of drawings. (Figure 2 is now two sheets instead of one.) The replacement drawings add no new matter and merely correct informalities in the drawings as originally submitted.